AMENDMENTS TO THE CLAIMS:

This listing of claims will replace all prior versions, and listings, of claims in the application.

Listing of Claims

1-46. (Cancelled)

47. (New) A method to select a cancer patient who is predicted to benefit from therapeutic administration of an EGFR inhibitor, an agonist thereof, or a drug having substantially similar biological activity as EGFR inhibitor, comprising:

a) providing a sample of tumor cells from a patient to be tested;

b) detecting in the sample the expression of one or more genes chosen from a panel of genes whose expression has been correlated with sensitivity or resistance to an EGFR inhibitor, wherein the one or more genes are chosen from a gene comprising, or expressing a transcript comprising, a nucleic acid sequence selected from the group consisting of SEQ ID NOs:1-194;

c) comparing the level of expression of the gene or genes detected in the patient sample to a level of expression of the gene or genes that has been correlated with sensitivity or resistance to the EGFR inhibitor; and

d) selecting the patient as being predicted to benefit from therapeutic administration of the EGFR inhibitor, if the expression of the gene or genes in the patient's tumor cells is statistically more similar to the expression levels of the gene or genes that has been correlated with sensitivity to the EGFR inhibitor than to resistance to the EGFR inhibitor.

48. (New) The method of Claim 47, comprising detecting expression of at least one gene selected from the group consisting of: E-cadherin (represented by SEQ ID NO:3) and ErbB3 (represented by SEQ ID NO:15 or SEQ ID NO:133).

49. (New) The method of Claim 47, comprising detecting expression of E-cadherin (represented by SEQ ID NO:3), wherein expression of E-cadherin in the patient's tumor cells is correlated with sensitivity to the EGFR inhibitor.

50. (New) The method of Claim 49, wherein detection of expression of E-cadherin in the patient's tumor cells indicates the ability to inhibit histone deacetylase HDAC in the tumor cells of the patient.

51. (New) The method of Claim 47, comprising detecting expression of at least one gene selected from the group consisting of ZEB1 and SIP1, wherein expression of ZEB1 or SIP1 in the patient's tumor cells is correlated with resistance to the EGFR inhibitor.

52. (New) The method of Claim 51, wherein detection of expression of ZEB1 or SIP1 in the patient's tumor cells indicates the recruitment of histone deacetylase HDAC in the tumor cells of the patient.

53. (New) The method of Claim 47, wherein the EGFR inhibitor is gefitinib.

54. (New) The method of Claim 47, wherein the step (b) of detecting comprises detecting expression of at least 10 genes in (b).

55. (New) The method of Claim 47, wherein expression of the gene or genes is detected by:

a) measuring amounts of transcripts of the gene in the tumor cells;

b) detecting hybridization of at least a portion of the gene or a transcript thereof to a nucleic acid molecule comprising a portion of the gene or a transcript thereof in a nucleic acid array; or

c) detecting the production of a protein encoded by the gene.

56. (New) The method of Claim 47, wherein the step of comparing comprises comparing the expression of the gene or genes to expression of the gene or genes in:

a) a cell from a non-cancerous cell of the same type;

b) an autologous, non-cancerous cell from the patient;

c) a control cell that is resistant to the EGFR inhibitor;

d) a control cell that is sensitive to the EGFR inhibitor; or

e) a predetermined level of expression of the gene or genes.

57. (New) A method to select a cancer patient who is predicted to benefit from therapeutic administration of an EGFR inhibitor, an agonist thereof, or a drug having substantially

similar biological activity as EGFR inhibitor, comprising selecting a patient with tumor cells expressing E-cadherin as predicted to benefit from therapeutic administration of the EGFR inhibitor, and selecting a patient with tumor cells expressing ZEB1 or SIP1 not predicted to benefit from therapeutic administration of the EGFR inhibitor.

58. (New) The method of Claim 57, wherein expression of E-cadherin in the patient tumor cells is compared to expression of E-cadherin in a control cell that is sensitive to the EGFR inhibitor.

59. (New) The method of Claim 57, wherein expression of ZEB1 or SIP1 in the patient tumor cells is compared to expression of ZEB1 or SIP1, respectively, in a control cell that is resistant to the EGFR inhibitor.

60. (New) A method to identify a compound with the potential to enhance the efficacy of EGFR inhibitors, comprising:

a) contacting a test compound with a cell that expresses at least one gene, wherein said gene is selected from any one of the genes comprising, or expressing a transcript comprising, a nucleic acid sequence selected from the group consisting of SEQ ID NOs:1-194;

b) identifying compounds selected from the group consisting of:

i) compounds that increase the expression or activity of the gene or genes in (a), or the proteins encoded thereby, that are correlated with sensitivity to gefitinib; and

ii) compounds that decrease the expression or activity of genes in (a), or the proteins encoded thereby, that are correlated with resistance to gefitinib;

c) wherein said compounds are identified as having the potential to enhance the efficacy of EGFR inhibitors.

61. (New) The method of Claim 60, wherein the cell expresses a gene encoding E-cadherin or ErbB3, and wherein step (b) comprises identifying compounds that increase the expression or activity of E-cadherin or ErbB3 or the gene encoding E-cadherin or ErbB3.

62. (New) The method of Claim 60, wherein the cell expresses a gene encoding ZEB1 and SIP1, wherein step (b) comprises identifying compounds that decrease the expression or activity of ZEB1 or SIP1 or the gene encoding ZEB1 or SIP1.

63. (New) The method of Claim 60, wherein the compound is identified as having the potential to inhibit histone deacetylase HDAC.

64. (New) The method of Claim 60, wherein the EGFR inhibitor is gefitinib.

65. (New) A method to treat a patient with a cancer, comprising administering to the patient a therapeutic composition comprising a compound that upregulates the expression or activity of E-cadherin or ErbB3 or the gene encoding E-cadherin or ErbB3 in the tumor cells of the patient or that downregulates the expression of ZEB1 or SIP1 or the gene encoding ZEB1 or SIP1 in the tumor cells of the patient.